

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Ashkenazi et al. Attorney's Docket No: 39780-2630P1C4

Serial No: 09/978,191 Group Art Unit: 1647

Filed: October 15, 2001 Examiner: O Hara, Eileen B

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents

P.O. Box 1450

Alexandria, Virginia 22313-1450

**DECLARATION OF AUDREY GODDARD, Ph.D.,
PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D.,
and WILLIAM I. WOOD, Ph.D.**
UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.
2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Holtzman *et al.*, U.S. Published Patent Application 20020028508, with effective priority date April 23, 1998 (09/065,363), and Sheppard *et al.*, U.S. Published Patent Application 20020028508, with effective priority date June 18, 1997 (09/050,143)
3. We conceived and reduced to practice the polypeptide comprising an amino acid sequence of residues 35-273 of SEQ ID NO:506 claimed in the above-identified application in the United States prior to June 18, 1997.
4. At the time the above polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA encoding the polypeptide comprising an amino acid sequence of residues 35-273 of SEQ ID NO:506.

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5. At the time the above polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was, and still is, responsible for overseeing the sequencing of nucleotides encoding novel polypeptides, including the polypeptide having an amino acid sequence of residues 35-273 of SEQ ID NO: 506 as claimed in the above-identified application.
6. At the time the nucleotide encoding the above polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was, and still is, responsible for overseeing the homology searches for novel polypeptides, including that for the polypeptide having an amino acid sequence of residues 35-273 of SEQ ID NO: 506 as claimed in the above-identified application.
7. A cDNA clone, referred to as DNA30943-1163 in the above-identified application, was identified as encoding the claimed polypeptide.
8. The full length sequence of the cDNA clone, DNA30943-1163, is shown in Figure 1 of the above-identified application. The amino acid sequence of the claimed polypeptide is shown in Figure 213 (residue 35-273 of SEQ ID NO: 506). The cDNA sequence encoding the claimed polypeptide has 722 nucleotide residues and is shown in Figure 212 (nucleotides 500-1222 of SEQ ID NO: 505) of the above-identified application. The claimed polypeptide has 238 amino acid residues, and is only slightly different from PRO213 at the N-terminal. That portion of PRO213, which overlaps with the claimed polypeptide of the above-identified application, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.
9. Copies of the pages from the GSeqEdit database which report the cloning, sequencing and functional data for the PRO213 polypeptide sequence, including its homology to human gas6, as well as the cloning, and sequencing data for the nucleic acid sequence encoding the PRO213 polypeptide are attached to this declaration (with the dates redacted) as Exhibit A. PRO213 comprises the amino acid sequence of residues 35-273 of SEQ ID NO: 506 as claimed in the present invention.
10. The GSeqEdit report shows the full-length nucleic acid sequence for DNA30943-1106 (identified as "DNA30943") and the full-length PRO213 polypeptide encoded

by DNA30943. Both the DNA30943 and the PRO213 polypeptide sequences and the homology of PRO213 to human gas6 were obtained prior to June 18, 1997.

11. The DNA sequence of nucleotides 498 to 1216 of the DNA 30943 sequence shown in the GSeqEdit report is identical to that of nucleotides 500-1222 of SEQ ID NO:505 disclosed in the above-identified application.
12. The beginning of the cDNA sequence corresponding to nucleotides 500-1222 of SEQ ID NO:505 in the above-identified application is shown on page 6 of the GSeqEdit database report. The location of nucleotide 500 of SEQ ID 505 is marked with an arrow. The location of the nucleotide 1222 of SEQ ID NO:505 is shown on page 12 and is marked with an arrow.
13. The sequence of amino acid residues 54 to 295 of PRO213 polypeptide shown in the GSeqEdit report is identical to that of amino acids 35-273 of SEQ ID NO: 506 disclosed in the above-identified application.
14. The amino acid residues 35 to 273 of SEQ ID NO: 506 are shown in the GSeqEdit report starting on page 6 and continuing until page 12 of the report.
15. Exhibit A clearly shows that both the amino acid sequence of amino acids 35 to 273 of SEQ ID NO: 506 and the nucleotide sequence encoding thereof disclosed in the above-identified application, as well as the homology of the claimed polypeptide to human gas 6 were obtained prior to **June 18, 1997**.
16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard

Date

Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date

William I. Wood, Ph.D.

Date

SV 2065805 v1
10/4/04 12:26 PM (39780.2630)

>Wednesday, September 22, 2004

>DNA30943 [Full]

>077 Sites All Sites

>[REDACTED] DNA30943, jean

> no stop in front

scrFI [M.hpaII-]
ncII
mspI
hpaII mnII
dsAV sau3AI rmaI
bssKI mbol/ndeII [dam-]
xmaI / pspAI maeI
smal dpmII [dam-]
scrFI [M.hpaII-]
rcII dpmII [dam+]
dsAV nlaiI xbaI sau3AI taqI
tsp509I [M.ecori-] bfaI mbol/ndeII [dam-]
ecori bssKI bstYI/xholI dpmII [dam-]
apoI bsaiI bamHI hpy18III mnII
bstNI mnII
bssKI [dam-] hoyCH4V
apyI [dam+] bsGI bsaiI taqI [M.claI-]
bsPDI [dam-] bsaiI alwI [dam-] dpmI [dam+]
claI/bsp106 avai [M.hpaII-] alwI [dam-] drdI
bsh1236I mnII bstYI/xholI mnII
bsPDI [dam-] bsaiI alwI [dam-] taqI mlwI ecII
bsGI caciI bsgI
1 CGAGGTCAA CTGCACTCTG GTCTATCGA TTGAATTCC CGGGGATTCCTC CTCGACATCC ACCCACGGT CGGCCTGCAC
GCTCCAGGT GACGTGGAGC CAAGATACT AACTTAAGG GCCCCTAEGA GATCTCTAGG GAGCTGGAGC TGGGGTGCAGA GGCGGACTGTG

XcmI								
scrFI [dcm-]								
DspGI	bsrI							sau96I [M.haeIII-]
MvaI	haeIII/palI							nlaIV
EcoRII [dcm-]								haeIII/palI
DsaV [dcm-]								eco01C9I/draIII
BspMI	ddeI							
ECORII [dcm-]	BspCM1	nlaIV						mnlI
DsaV [dcm-]	mnlI	mnlI						ddeI
BstXI [M.haeIII-]	hpv198III							bspCNI
BstNI								bsu36I/mstIII/sauI
HpaCH4V								bsu36I/mstIII/sauI
TseI	nlaIV							rmaI
Znu4HI/bsoFI								mciI
BbvI	mnlI							bfaI
1.01	GGCTGCAGG GAGGCAAGTC TGGACAGGCC AGCTCAGGAG GTGCCCTCAG CCCAGCAAGG GC ["] AGGTCC CGGAGCTCC CTCGAGEAC ACCTGTCGG ACCGACGTCAC CGCCGGTCAC CACGGAGGTG CGATCCCCAGG							

GSeqEdit, DNA30943 [Full], page 3

GseqEdit, DNA30943 [Full], page 4

bsaXI

:thIII/aspl

pflPI

sau96I

nlaIV

avaII

sanDI

ppuMI

tseI

fnu4HI/bsoFI

nlaIV

hpy188I

pieI

bbvI

hpyCH4V

rsal

hphi

bsII

bsp1286

sa96I

[M.haeIII-]

bsmFI

bstAI

hinfI

bsqI

csp6I

mnlI

bspMI

bmyI

bssKI

pstI

[M.HI-]

bsII

501 GCTCACGGGG ACCCTCTCTC CGAGTCGTC TGACCAAGGTG
CGAGTGCCCC TGGGACAGAG GCTCACCAAG CACGTCGAC ACATGTCGG
35 A H G D P V S E S F V Q R V Y Q P F L T T C D G H R A C S T Y R T I

scrFI [dcm-]		sau96						
pspGI	staiI [dcm-]	nlary						
rvaI	scrI [dcm-]	scrFI [dcm						
ecoriI [dcm-]	pspGI	pspGI						
dsav [dcm-]	rvaI							
bstNI	ecoriI [dcm-]	thaI	rspl					
bssKI [dcm-]	dsav [dcm-]	fudII/mvnI	hpaiI					
bsI	bstNI	bstII	tseI	scrII [M. hpaII-]				
tseI bsaji	sau96I [M. haeIII-]	osh1236I	ncII	sau96I	bstNI			
fnu4HI/bsoFI	nlarV	bssKI [dcm-]	mluI	mwol	dsav	bskI [dcm		
aciI	bsaJI	haeIII/palI	haeIII/palI	fnu4HI/bsoFI	avall	cac8I	bsaJZ mwO	
aciI	fnu4H-/bscFI	cac8I	apYI [dcm+]	aflIII	bbvI	bssKI	mspAII/mspBII	ec0010
sau96I	aciI	bboVI	apYI [dcm+]	rnII	mwol	cac8I	earI/ksp632I	apYI [dcm+
sclI	avaiI	bsII [dcm+]	bsII [dcm-]	bsaJI	earI/ksp632I			
601	TCATAGGNC	CGGCCTACCCSC	GGCTGGCCC	GGCTACGGGT	GGTGCCTGGGT	CIGGAGGG	ACCAAGGGGG	TGCCCTGGGG
	AGATAATCCTG	GCGGATGGCG	GGGTCTGGAC	ACGGTCCGA	GGCATGCGCA	CGACGGGGCC	GACCTCTCC	TGGTGCCCCG
69	Y R T A Y R R S P G L A P A R P R Y A C C P G W K R T S G L P G A							

^edit T to C, does not charge aa -goddard 6/8/98

scrFI [dcm-]
 pspGI
 mvaI
 ecoRII [dcm-]
 dsaV [dcm-]
 bstNI
 sau36I [M. haeIII-]
 nlaIV bssK1 [dcm-]
 haelli/palI
 sau96I [M. haeIII-]
 pspOMI/bsp12CI
 nlaIV bsaJI
 eco0109I/draII
 bsp1286 [M. haeIII-]
 bmyI apyI [dcm+]
 banII [M. haeIII-]
 styI
 bstII
 draII:
 bsp1286 apal bsaJI sau96I [M. haeIII-]
 bmyI bsaJI eco0109I/draII nlaIV
 sfiI csp6I bsp14CI/hpyCH4III bsp14CI/hpyCH4III
 bstI bst4CI/hpyCH4III bsp14CI/hpyCH4III
 9C1 GCCTGGTGC AGACGGTACA CCTCTGTGC CCAAGGGAGG GCCCCCCCACGG GTGGCACAGT GCATGAAAGG ARGAAGTGCA
 CGGACAGACCG TCTGCCATGT GAGAACACAGG GGTTCCCTCC CGGGGGTCC CACCGGGGGT TGGGCTGTCC TCACCTGTCA CGTTACITTC TTCTTCACGT
 169 L S A D G T L C V P K G G P P R V A P N P T G V D S A M K E E V Q

hgiA- / aspE I

bspI 206

bsi:HAI

bnvI

scrF [dcm-]

tseI

gspG-

fnu4HI/bsoFI

bboV-

nvaI hpyCH4V

mspI ecoRII [dcm-]

hpaII

dsav [dcm-]

scrFI [N.hpaII-] apalI / snoI

ncI I

bscKI [dcm-]

dsav

bskII

apyI [dcm-]

bsaI

mnII alw49I / snoI

bsaI

mnII

scrF [dcm-] tseI gspG- fnu4HI/bsoFI acII fnu4HI/bscrI ncrI pI I eagI/xmaII/eclXI eaeI mlyI aluI haelli/palI cac8I tseI cfri hinfi [M.taqI-] fnu4HI/bsoFI taqI ddeI bbvi bspCNI bspCNI sfaNI bspCNI ddeI apyI [dcm+] msPAlI/msPBII gacACTCCCTGC CAGGAGCTTG GCGGATCGA CCTCCCTGAGC GACCGAGATT CCTGCTCAA GGAGGACCT CCTGTCGAC CCCAGGGACCA
110: GACCCCEGCA GCCTCCRGGT GCACTCCCTC CAGGAGCTTG GCGGATCGA CCTCCCTGAGC GACCGAGATT CCTGCTCAA GGAGGACCT CCTGTCGAC CCCAGGGACCA
CTGGGGCTT CGGGGACCA CGTGAACGAG GTCTGAGAG CTGGGACTCG CTGGGACTCT GAGGGACTCT CCTGCTCAA GGAGGACCT CCTGTCGAC CCCAGGGACCA
235 2 G S - I V H S F Q Q L G R I D S L S E Q I S F L E E Q L S S C S

scrFI [dcm-]
 pspGI
 mvaI
 ecoRII [dcm-]
 dsav [dcm-]
 bstNI mwol fnu4HI/dsoFI
 bslI bsp1286 bbvI
 mwol bssKI [dcm-] bmyI hpy1
 p-eI tsp45I hinPI apyI [dcm+] banII sfcI nsphi
 mlYI maellI hhaI/cfo⁻ ddeI actI PstI [M.H1-] bstXI sau96I
 avall
 hoyCH4V raeII bsauII bspCNI mn1I fnu4HI/bsoFI mlAII nspl mlAIV
 1201 CCTGCAAGAA AGACTGTGA CTGGCCAGCG CCCAAGGGCTG GACTGAGGCC CTCACCCGC CCTGCAGGCC CCATGCCCC CCTGCAGCATG CTGGGGGCC
 GGACCTTCTT TCTGAGCACT GACGGGTGCG GGGGTCCGAC CTGACTCGGG GAGTGCAGGG GGACGTGGG GGTAGGGGA CGGTGTGAC GACCCAGG
 269 C K D S O

scrFI [dcm-]						
pspGI						
rvaI						
ecoriI [dcm-]						
csaIV [dcm-]						
bstNI						
bssKI [dcm-]						
bsI I [dcm-]						
apyI [dcm+]						
bsI I						
bsaVI						
alwNII [dcm-]						
scrFI [dcm-]						
pspGI	haeIII/palI					
mvaI	sau96I [M.haeIII-]					
ecoriI [dcm-]						
dsaIV [dcm-]	earI/ksp632I					
bstNI eco0109I/draII						
bsaVI	ddeI					
mnlI	tsp45I acI I	bskI [dcm-]	mnlI	bseRI	mnlI	
bsaVI	maeIII bsrBI	apyI [dcm+]	bseRI	mnlI	bsI I	alw26I/bsmAI
bsI I	hpI I bsgCNI	haeIII/palI	mnlI	mboII	mnlI	pflMI [dcm-]
			mnlI	bsI I	bsaVI	bsI I [dcm-]
						mlaII
						mlaIV
						mlaV
						mlaVI
						fok
						bst
301 AGAGCCACC TGGGGTGCAC TGAGGGGAG GCGAGGCCAG GCCTTCCTTC TCTTCCTCTT CCCCCTTCCTT CCGAGGGCTCC CCAGACCCCTG GCATGGGA TCTTGGGG AGAAGGAGGA CGGAGGGG AGAAGGAGGA CGCTCCGGGG CCTCTCCGTC CGGTCCGTC CGTACCCCT						

^deleted a C -goddara 6/8/98
edit G to C -goddarda 6/8/98

edit T >o C -goddarda 6/8/98
^edit T to C -goddarda 6/8/98
^edit T to C -goddarda 6/8/98

sau96I

n.lay

avaI

sarDI

ppMI

nlayV

eco01C9I/draII

scrFI [dcm-]

pspG-

nlaIII-

ecoriI [dcm-]

nvaI

styI

dsavI [dcm-]

dstNI

ncoI

bsSKI [dcm-]

bsaI

dsal

apyI [dcm+]

nlaIV

bamHI

btgI/bstDSI

bsaX-

nlaIV

bspQNI

nlaIV

tspRI

tseI

bsaI

bsaII

bsaIII

bsaIV

bsaV

bsaVI

bsaVII

bsaVIII

bsaIX

bsaXI

tseII

bsaXI

bsaXII

bsaXIII

bsaXIV

bsaXV

bsaXVI

bsaXVII

bsaXVIII

bsaXIX

bsaXX

bsaXXI

bsaXXII

bsaXXIII

bsaXXIV

bsaXXV

bsaXXVI

bsaXXVII

bsaXXVIII

bsaXXIX

bsaXXX

bsaXXI

bsaXXII

bsaXXIII

bsaXXIV

bsaXXV

bsaXXVI

bsaXXVII

bsaXXVIII

bsaXXIX

bsaXXX

bsaXXI

bsaXI

tseII

bsaXI

bsaXII

bsaXIII

bsaXIV

bsaXV

bsaXVI

bsaXVII

bsaXVIII

bsaXIX

bsaXX

bsaXXI

bsaXXII

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bsaXXI

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bsaXXVIII

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bsaXX

bsaXXI

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bsaXXVII

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bsaXXIX

bsaXXX

bsaXXI

bsaXXII

bsaXXIII

bsaXXIV

bsaXXV

bsaXXVI

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bsaXXVIII

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bsaXXVIII

bsaXXIX

bsaXXX

bsaXI

tseII

bsaXI

bsaXII

bsaXIII

bsaXIV

bsaXV

bsaXVI

bsaXVII

bsaXVIII

bsaXIX

bsaXX

bsaXXI

bsaXXII

bsaXXIII

bsaXXIV

bsaXXV

bsaXXVI

bsaXXVII

bsaXXVIII

bsaXXIX

rnaI					
mael					
	pieI				
	acII	mYI	sa		
	fnu4HI/bsoFI		stYI		
	maeIII/palI		acII	ha	
	hinFI	taqI	mwI	nlAI	
	eaGI/xmaIII/ecXI	saiI	fnu4HI/bso		
	eaEI	xbal	palI	stII	mcoI [M
	cfRI	fnuDII/mvaI	hinCI/hindII	[M.taqI-]	dsal
	baIEI	drdI	mlYI	psI	dtgI/b
	notI	bstUI	mpy188III	bspMI	bsaJI
	acII	bsh1236I	hinFI/M.taqI-1	aluI	haeIII/pal-
	taII	maeIII	hndIII	baeI	
	maeII/hpyCH4IV	aaaaaaa	aaaaaaa	aa	
1601	ATGAACT	AAAGGGCGGC	GGCGACTTA	GAGTCGACCT	GCAGAAGCTT
	TCTTTGCA	CTTTTTT	TTTTTTT	GGGTGAGAT	GGCCGCCATG
				CTCAGCTGA	CGTCTTCGAA
					CGGGGGTAC
	aluI				
	tsel				
	fnu4HI/bsoFI				
	bbvI	psI			
	hpyCH4V		maeIII		
1701	GCCCACTTG	TTTATGCAG	CTTATAATGG	TTACAAAT	
	CGGGTTAAC	AAATAACGT	GAATAATTAC	ATGTTTA	

> Length: 1738

acc65-(GGTACCI) :

1447

The screenshot shows a search interface for 'DNA30943'. At the top, there are tabs for 'GENE360ES', 'SEARCH', 'MAP', 'Additional Resources', and 'HELP'. Below the tabs are several search filters: 'Species' (Human), 'Gene ID' (DNA30943), 'Protein ID' (NP_016215), 'Chromosome' (18), 'Start' (123456789), 'End' (123456789), 'Strand' (+), 'Gene Type' (Protein-coding), 'Organism' (Homo sapiens), 'Tissue' (Fetal Lung), 'Cell Type' (None), 'Protein Function' (None), 'Protein Subunit' (None), 'Protein Complex' (None), 'Protein Interaction' (None), 'Protein Post-translational Modification' (None), 'Protein Expression' (None), 'Protein Localization' (None), and 'Protein Activity' (None). There are also buttons for 'Find', 'New', 'Update', 'Select', and 'Go'.

DNA30943

DNA Info [Project DNA28735](#)Is PrimaryDNA

Source Info 187 FLS 339 LIB25 RNA22 SRC18 Human Fetal Lung

Gene Info [PRO21.1](#) Human Egfl7 (VEMF) Non-Secreted UNQ187**Gene Annotation**

Genome Mapping Run Geode

Affy [HGU133A_218825_at](#)[HGU133P_218825_at](#)[HGU95C_48695_at](#)[Hu35KA_R39467_f_at](#)[Hu35KC_RC_N74688_f_at](#)[Hu35KD_RC_N70081_at](#)[HuGenet1_NM_016215_at](#)[MOE430A_1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at](#)[MOE430P_1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at](#)[Rat230v2_1370402_at, 1374570_at, 1393427_s_at](#)Agilent [H1Av2_A_23_P123785](#)[H1A_A_23_P123785](#)[H1Av2_A_23_P123785](#)[H1B_A_32_P210642, A_32_P300230](#)[M1A_A_51_P315841](#)[WHG_A_32_P210642](#)FANTOM [Mouse:0610012G11](#)

Human:AB125649, AF186111, AL512735, AY358901, AY358902, AY358903, BC012377

GenBank [Mouse:AF184973, AK002601, AY239289, AY239290, AY309459, BC024610](#)

GeneHub Human:GENE7437

Mouse:MGENE1470

INCYFL Human:931424.FL1_0, 931424.FL3_0

Incyte Human:416842.1, 416842.13, 416842.17, 416842.56, 416842.58, 416842.62, 416842.64, 416842.67, 416842.68
416842.69, 416842.70, 416842.72, 416842.74, 984053.1

LocustLink Human:51162

Mouse:353158

MGI [Mouse:2449923](#)

OMIM Human:608582

Proteome Human:NP_958854.1

Mouse:NP_942017.1

RefSeq Human:NM_016215, NM_201446

Mouse:NM_178444, NM_198724, NM_198725

UniGene Human:Hs.91481

Mouse:Mr.268933

General Info

Lab Name 28735.2

Insert (Digest) Size(bp) 1600

Insert Name undetermined

Reverse Size(bp) 1

Generated By Full Length Screen

Internal Size(bp) 239

Type of DNA FLS

Cut Size(bp)

Insert ID Novel

Vector

Action Dp Not FL

Interest not reviewed

Concentration

Origene CloneID

Origene Plate

Origene Well

Construct Info

Exp System

Tag

Sequence Status

Bases to Sequence

Antibody Info No antibody infoOther Info In Situ image available TaqMan Hit Transgenic Animal Model

	OLI5288	
	OLI5289	
	OLI5290	
	OLI5572	30943.f1
Oligos	OLI5573	30943.f2
	OLI7839	30943.tm.f1
	OLI7840	30943.tm.r1
	OLI7841	30943.tm.p1
	OLI7845	30943.tm.f3
	OLI7846	30943.tm.r3
	OLI7847	30943.tm.p3

Comments

Login	Date Entered	Annotation
dtb	[REDACTED]	homolog to an unknown human protein and to gas6. The mouse protein with 40 % identity clearly has a signal sequence wheras this clone does not. I think the clone is suspect.-ALG
goddarda	[REDACTED]	Sequencing in clone 64908 allowed us to correct three sequencing errors in 30943 which lie in the 5' UTR of the gene. However the presence of these errors caused us to identify the wrong 5' end of the ORF in the gene. -goddarda
goddarda	[REDACTED]	Sequence was flagged as poor quality during proofreading. Tried to rerun reactions with Big DYE chemistry, but too little DNA - signal unreadable. Requested more DNA 2/98. Never received -goddarda
goddarda	[REDACTED]	amplified colon tumors and to a lesser extent in lung tumors- TaqMan assay
jean	[REDACTED]	Clone 30943 from plasmid inventory plate is verified correct through partial sequencing

Legal Status No legal status

Status

Scientist Daryl Baldwin

Notebook 0

Date Entered A [REDACTED]

Date Updated February 14, 2003

Page

Date Completed

Storage Location

Date Canceled

Box

Cancel Reason

Slot

Clone Status not reviewed

Inventory Status

Sequence Status

Others Sent to pLASMID Archive
 Clone Verified

Project Member

No Project member generated

FLS FLSDNA

No FLS, FLSDNA generated

Exp Construct

EXP	Lab Name	Construct DNA	System
<u>EXP7559</u>	Protein Engineering	<u>DNA348527</u>	Baculovirus

ABI

ABI Run Lane Date Sequenced ABI Plate

ABI512.31	04/07/1997
ABI512.32	04/07/1997
ABI512.33	04/07/1997
ABI512.34	04/07/1997
ABI512.35	04/07/1997
ABI812.30	10/06/1997
ABI812.31	10/06/1997
ABI1055.40	02/10/1998
ABI1055.41	02/10/1998
ABI2530.13	02/11/2000

1252

MA Plate

MA Plate	Well Num	Well Location	Date	Type Plate
<u>PLT129</u>	25	C1	08/11/1999	Inventory

Print Run

No Print run generated

XPT

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